

# Sequence alignment for 10/527,469

US-08-813-150-4  
; Sequence 4, Application US/08813150  
; Patent No. 6069229  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Christopher  
; APPLICANT: Lebecque, Serge J.E.  
; APPLICANT: Liu, Yong-Jun  
; APPLICANT: Dowling, Lynette M.  
; APPLICANT: Huffine, Constance M.  
; APPLICANT: Gorman, Daniel M.  
; TITLE OF INVENTION: MAMMALIAN PROTEINASES; OXIDOREDUCTASES;  
; TITLE OF INVENTION: RELATED REAGENTS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/813,150  
; FILING DATE: 07-MAR-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
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; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: SF0693  
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; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 567 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-813-150-4

Query Match 100.0%; Score 567; DB 2; Length 567;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLPALHLHLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTVGLNRTLKPQ	60
Db	1	MLPALHLHLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTVGLNRTLKPQ	60
Qy	61	RVIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPS	120
Db	61	RVIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPS	120
Qy	121	HRILHLKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKVPKLGALRPQEGHGSPE	180
Db	121	HRILHLKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKVPKLGALRPQEGHGSPE	180

Qy 181 DIYQMALNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFY 240  
 |||  
 Db 181 DIYQMALNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFY 240  
 |||

Qy 241 LSF AEALRAHSCLSDR LQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGP HDVHVQ 300  
 |||  
 Db 241 LSF AEALRAHSCLSDR LQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGP HDVHVQ 300  
 |||

Qy 301 IETSPPARNLKVLKADVLLTASGPAVKRITFSPLPRHMQEALRRLHYVPATKVFLSFR 360  
 |||  
 Db 301 IETSPPARNLKVLKADVLLTASGPAVKRITFSPLPRHMQEALRRLHYVPATKVFLSFR 360  
 |||

Qy 361 RPFWREEHIEGGHSENTDRPSRMIFYPPPREGALLASYTWSDA AAFAGLSREEALRLAL 420  
 |||  
 Db 361 RPFWREEHIEGGHSENTDRPSRMIFYPPPREGALLASYTWSDA AAFAGLSREEALRLAL 420  
 |||

Qy 421 DDVAALHGPVVRQLWDGTGVV KRWAEDQHSQGGFVVOPPALWQTEKDDWTVPYGRIYFAG 480  
 |||  
 Db 421 DDVAALHGPVVRQLWDGTGVV KRWAEDQHSQGGFVVOPPALWQTEKDDWTVPYGRIYFAG 480  
 |||

Qy 481 EHTAYPHGWVETAVK SALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVA SPSHD 540  
 |||  
 Db 481 EHTAYPHGWVETAVK SALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVA SPSHD 540  
 |||

Qy 541 LAKEEGSHPPVQGQLSLQNTTHTRTSH 567  
 |||  
 Db 541 LAKEEGSHPPVQGQLSLQNTTHTRTSH 567  
 |||